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I hereby certify under 37 C.F.R. § 1.8(a) that this correspondence is being deposited with the United States Postal Service as **first class mail** with sufficient postage on the date indicated above and is addressed to Mail Stop AF, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Tracy Simmons

Printed name of person mailing correspondence

Tracy Simmons

Signature of person mailing correspondence

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Roy A. Gravel et al. Art Unit: 1632

Serial No.: 09/487,841 Examiner: Shin-Lin Chen

Filed: January 19, 2000 Customer No.: 21559

Title: HUMAN METHIONINE SYNTHASE REDUCTASE: CLONING, AND METHODS FOR EVALUATING RISK OF, PREVENTING, OR TREATING NEURAL TUBE DEFECTS, CARDIOVASCULAR DISEASE, CANCER, AND DOWN'S SYNDROME

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STATEMENT UNDER 37 C.F.R. § 1.821

Enclosed is a Sequence Listing in accordance with the requirements of 37 C.F.R. §§ 1.821 through 1.825 and consisting of 28 pages.

As required by 37 C.F.R. § 1.821(c), the Sequence Listing appears as a separate part of the application. Each sequence in the application appears separately in the Sequence Listing, and each sequence in the Sequence Listing is assigned a separate sequence identifier.

As required by 37 C.F.R. § 1.821(d), the sequence identifiers are used throughout

the application description and claims to refer to their respective sequences.

As required by 37 C.F.R. § 1.821(e), enclosed is a diskette containing a copy of the Sequence Listing in computer readable form.

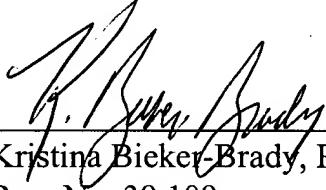
As required by 37 C.F.R. § 1.821(f), I hereby state that the contents of the computer readable form of the Sequence Listing are the same as the contents of the paper copy.

As required by 37 C.F.R. § 1.821(g), I hereby state that this submission contains no new matter.

If there are any charges or any credits, please apply them to Deposit Account No. 03-2095.

Respectfully submitted,

Date: December 15, 2004


Kristina Bieker-Brady, Ph.D., P.C.
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SEQUENCE LISTING

<110> Gravel, Roy A,
Rozen, Rima
Leclerc, Daniel
Wilson, Aaron
Rosenblatt, David

<120> HUMAN METHIONINE SYNTHASE REDUCTASE:
CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
DEFECTS, CARDIOVASCULAR DISEASE, CANCER, AND DOWN'S SYNDROME

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<151> 1999-08-10

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Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
50 55 60
Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
65 70 75 80
Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
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Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
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Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
115 120 125
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130 135 140
Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
145 150 155 160
Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
165 170 175
Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
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Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
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Ser Leu Gly Gln Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro
260 265 270

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 Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
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 Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
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 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
 485 490 495
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 580 585 590
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Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
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Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
85 90 95
Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
100 105 110
Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
115 120 125
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130 135 140
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145 150 155 160
Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
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Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
 180 185 190
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 Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu

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 Thr Glu Lys Ile Asn Ala Gln Ile Pro Gly His Val His Lys Ile Thr
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 Glu Lys Arg Arg Leu Leu Glu Leu Cys Ser Ala Gln Gly Met Lys Asp
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 Ala Ser Thr Glu Ser Lys Ile Phe Ile Cys Gly Asp Ala Lys Gly Met
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Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp			
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Asp Gly Asn Leu Glu Asp Phe Ile Thr Trp Arg Glu Gln Phe Trp			
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Pro Ala Val Cys Glu His Phe Gly Val Glu Ala Thr Gly Glu Glu Ser			
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Ser Ile Arg Gln Tyr Glu Leu Val Val His Thr Asp Ile Asp Ala Ala			
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Ile Leu Gly Ala Asp Leu Asp Val Val Met Ser Leu Asn Asn Leu Asp			
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Glu Glu Ser Asn Lys Lys His Pro Phe Pro Cys Pro Thr Ser Tyr Arg			
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His Pro Asn Ser Val His Ile Cys Ala Val Val Val Glu Tyr Glu Thr			
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 Gln Glu Arg Ala Trp Leu Arg Gln Gln Gly Lys Glu Val Gly Glu Thr
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 Glu Glu Leu Ala Gln Phe His Arg Asp Gly Ala Leu Thr Gln Leu Asn
 580 585 590
 Val Ala Phe Ser Arg Glu Gln Ser His Lys Val Tyr Val Gln His Leu
 595 600 605
 Leu Lys Gln Asp Arg Glu His Leu Trp Lys Leu Ile Glu Gly Gly Ala
 610 615 620
 His Ile Tyr Val Cys Gly Asp Ala Arg Asn Met Ala Arg Asp Val Gln
 625 630 635 640
 Asn Thr Phe Tyr Asp Ile Val Ala Glu Leu Gly Ala Met Glu His Ala
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 <212> DNA
 <213> Homo sapiens

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<400> 26
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<210> 27
<211> 18
<212> PRT
<213> Oryctolagus cuniculus

<400> 27
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<210> 28
<211> 18
<212> PRT
<213> Drosophila melanogaster

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<210> 29
<211> 18
<212> PRT
<213> Vigna radiata

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<210> 30
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<212> PRT
<213> Aspergillus niger

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<210> 31
<211> 18
<212> PRT
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<210> 32
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<400> 33
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<210> 34
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<212> PRT
<213> Oryctolagus cuniculus

<400> 34
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1 5 10 15
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<210> 35
<211> 18
<212> PRT
<213> Gallus gallus

<400> 35
Gly Asp Met Ile Leu Leu Phe Gly Cys Arg His Pro Asp Met Asp His
1 5 10 15
Ile Tyr

<210> 36
<211> 18
<212> PRT
<213> Escherichia coli

<400> 36

Gly Lys Asn Trp Leu Phe Phe Gly Asn Pro His Phe Thr Glu Asp Phe
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Leu Tyr

<210> 37
<211> 18
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 37
Gly Glu Val Phe Leu Tyr Leu Gly Ser Arg His Lys Arg Glu Glu Tyr
1 5 10 15
Leu Tyr

<210> 38
<211> 18
<212> PRT
<213> *Thiocapsa roseopersicina*

<400> 38
Gly Arg Asn Trp Leu Ile Phe Gly Asn Arg His Phe His Arg Asp Phe
1 5 10 15
Leu Tyr

<210> 39
<211> 19
<212> PRT
<213> *Pisum sativum*

<400> 39
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<210> 40
<211> 18
<212> PRT
<213> *Spinacia oleracea*

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<210> 41
<211> 2097
<212> DNA

<213> Homo sapiens

<400> 41

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<210> 42

<211> 698

<212> PRT

<213> Homo sapiens

<400> 42

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Ala	Asp	Leu	His	Cys	Ile	Ser	Glu	Ser	Asp	Lys	Tyr	Asp	Leu	Lys	Thr
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Glu	Thr	Ala	Pro	Leu	Val	Val	Val	Val	Ser	Thr	Thr	Gly	Thr	Gly	Asp
					50			55			60				
Pro	Pro	Asp	Thr	Ala	Arg	Lys	Phe	Val	Lys	Glu	Ile	Gln	Asn	Gln	Thr
					65			70			75			80	
Leu	Pro	Val	Asp	Phe	Phe	Ala	His	Leu	Arg	Tyr	Gly	Leu	Leu	Gly	Leu
					85			90				95			

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 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
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 130 135 140
 Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
 145 150 155 160
 Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
 165 170 175
 Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
 180 185 190
 Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
 195 200 205
 Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe
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 Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu
 225 230 235 240
 Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu
 245 250 255
 Ser Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro
 260 265 270
 Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
 275 280 285
 Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
 290 295 300
 Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
 305 310 315 320
 Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
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 Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
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 Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
 355 360 365
 Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
 370 375 380
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 385 390 395 400
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 405 410 415
 Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
 420 425 430
 Ser Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu
 435 440 445
 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
 450 455 460
 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
 465 470 475 480
 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
 485 490 495
 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
 500 505 510
 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
 515 520 525
 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
 530 535 540
 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu

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565	570	575	
Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu			
580	585	590	
Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser			
595	600	605	
Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr			
610	615	620	
Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu			
625	630	635	640
Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met			
645	650	655	
Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val			
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Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu			
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Glu Lys Arg Tyr Leu Gln Asp Ile Trp Ser			
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<210> 43
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<212> DNA
<213> *Homo sapiens*

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<210> 44
<211> 698
<212> PRT
<213> Homo sapiens

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35 40 45
Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
50 55 60
Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
65 70 75 80
Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
85 90 95
Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
100 105 110
Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
115 120 125
Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
130 135 140
Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
145 150 155 160
Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
165 170 175
Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
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Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
195 200 205
Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe
210 215 220
Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu
225 230 235 240
Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu
245 250 255
Ser Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro
260 265 270
Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
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Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
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Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
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Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
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Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
340 345 350
Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe

355	360	365
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465	470	475
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Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu		
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Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser		
595	600	605
Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Ala Pro Ala Lys Tyr		
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Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu		
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Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met		
645	650	655
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Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val		
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Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu		
675	680	685
Glu Lys Arg Tyr Leu Gln Asp Ile Trp Ser		
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<211> 2094
<212> DNA
<213> Homo sapiens

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 gcaaagtatg tacaagacaa catccagctt catggccagc aggtggcag aatcctcctc 1920
 caggagaacg gccatattt tttgtgttgc gatgcaaaga atatggccaa ggatgtacat 1980
 gatgccctt gtcataataa aagcaaagag gttggagttt aaaaactaga agcaatgaaa 2040
 accctggcca ctttaaaaga agaaaaacgc tacttcagg atatttggtc ataa 2094

<210> 46
 <211> 697
 <212> PRT
 <213> Homo sapiens

<400> 46
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 Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
 35 40 45
 Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
 50 55 60
 Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
 65 70 75 80
 Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
 85 90 95
 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
 100 105 110
 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
 115 120 125
 Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
 130 135 140
 Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
 145 150 155 160
 Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg

165	170	175
Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu		
180	185	190
Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys		
195	200	205
Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe		
210	215	220
Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu		
225	230	235
Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu		
245	250	255
Ser Leu Gly Gln Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro		
260	265	270
Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp		
275	280	285
Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp		
290	295	300
Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser		
305	310	315
Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys		
325	330	335
Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys		
340	345	350
Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe		
355	360	365
Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe		
370	375	380
Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg		
385	390	395
Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe		
405	410	415
Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro		
420	425	430
Ser Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu		
435	440	445
Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly		
450	455	460
Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr		
465	470	475
Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu		
485	490	495
Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser		
500	505	510
Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn		
515	520	525
Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly		
530	535	540
Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu		
545	550	555
Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Phe		
565	570	575
Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu Leu		
580	585	590
Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser Phe		
595	600	605
Ser Arg Asp Ala Pro Val Gly Glu Glu Ala Pro Ala Lys Tyr Val		
610	615	620

Gln	Asp	Asn	Ile	Gln	Leu	His	Gly	Gln	Gln	Val	Ala	Arg	Ile	Leu	Leu
625				630				635				640			
Gln	Glu	Asn	Gly	His	Ile	Tyr	Val	Cys	Gly	Asp	Ala	Lys	Asn	Met	Ala
				645				650				655			
Lys	Asp	Val	His	Asp	Ala	Leu	Val	Gln	Ile	Ile	Ser	Lys	Glu	Val	Gly
				660				665				670			
Val	Glu	Lys	Leu	Glu	Ala	Met	Lys	Thr	Leu	Ala	Thr	Leu	Lys	Glu	Glu
				675				680				685			
Lys	Arg	Tyr	Leu	Gln	Asp	Ile	Trp	Ser							
				690				695							

<210> 47
 <211> 2093
 <212> DNA
 <213> Homo sapiens

<400> 47

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 tccgataagt atgacctaaa aaccgaaaca gctcctctt ttgtgtggg ttctaccacg 180
 ggcaccggag acccaccgcg cacagccgc aagttgtta agaaaataca gaaccaaaca 240
 ctgcgggtt atttcttgc tcacctgcgg tatgggtac tgggtctcg tgattcagaa 300
 tacacctact ttgcataatgg gggaaagata attgataaac gacttcaaga gttggagcc 360
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 gaggagataa gtggcgcaact cccggatggca tcacctgcatt ccttggaggac agaccttgc 540
 aagtccagacg tgctacacat tgaatctcaa gtcgagcttc tgagattcga tgattcagga 600
 agaaaaggatt ctgagggtttt gaagcaaaat gcagtgaaca gcaaccaatc caatgttgc 660
 attgaagact ttgagtcctc acttacccgt tcggtaaaaa cactctcaca agcctctctg 720
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 ccctggccac tttaaaagaa gaaaaacgct accttcagga tatttggtca taa 2093

<210> 48
 <211> 689
 <212> PRT

<213> Homo sapiens

<400> 48
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20 25 30
Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr Glu
35 40 45
Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp Pro
50 55 60
Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr Leu
65 70 75 80
Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu Gly
85 90 95
Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp Lys
100 105 110
Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His Ala
115 120 125
Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala Gly
130 135 140
Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln Glu
145 150 155 160
Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg Thr
165 170 175
Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu Leu
180 185 190
Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys Gln
195 200 205
Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe Glu
210 215 220
Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu Asn
225 230 235 240
Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu Ser
245 250 255
Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro Val
260 265 270
Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp Ala
275 280 285
Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp Phe
290 295 300
Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser Asp
305 310 315 320
Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys Arg
325 330 335
Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys Gly
340 345 350
Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe Ile
355 360 365
Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe Leu
370 375 380
Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg Leu
385 390 395 400
Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe Val
405 410 415
Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro Ser
420 425 430

Cys Gln Pro Pro Leu Ser Leu Leu Glu His Leu Pro Lys Leu Gln
 435 440 445
 Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly Lys
 450 455 460
 Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr Thr
 465 470 475 480
 Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu Val
 485 490 495
 Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser Gly
 500 505 510
 Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn Ser
 515 520 525
 Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly Pro
 530 535 540
 Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Asn Ser
 545 550 555 560
 Lys Asn Asn Thr Gln Met Glu Ile Leu Glu Gln Cys Gly Cys Phe Leu
 565 570 575
 Ala Ala Gly Ile Arg Ile Gly Ile Ile Tyr Ser Glu Lys Ser Ser Asp
 580 585 590
 Ile Ser Leu Ser Met Gly Ser Leu Ile Arg Phe Pro Ser Gln Glu Met
 595 600 605
 Leu Leu Leu Gly Arg Arg Lys Pro Gln Gln Ser Met Tyr Lys Thr Thr
 610 615 620
 Ser Ser Phe Met Ala Ser Arg Trp Arg Glu Ser Ser Ser Arg Arg Thr
 625 630 635 640
 Ala Ile Phe Met Cys Val Glu Met Gln Arg Ile Trp Pro Arg Met Tyr
 645 650 655
 Met Met Pro Leu Cys Lys Ala Lys Arg Leu Glu Leu Lys Asn Lys Gln
 660 665 670
 Lys Pro Trp Pro Leu Lys Lys Lys Asn Ala Thr Phe Arg Ile Phe Gly
 675 680 685
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<210> 49
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 49
 gcaaaggcca tcgcagaaga cat

23

<210> 50
 <211> 26
 <212> DNA
 <213> Homo sapiens

<400> 50
 gtgaagatct gcagaaaatc catgta

26

<210> 51
 <211> 2187
 <212> DNA
 <213> Homo sapiens

<400> 51
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gagggccatg agagactccg ggagaagatg aggccggcat tggatctgg tgacaagtgg 180
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gaccctggct cagacaagga gaccccttcc atgatgatcg ccagcaccgc cgtgaactac 360
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catggaaacc tagtactctc tgctcta 2187

<210> 52
<211> 20
<212> PRT
<213> *Homo sapiens*

<400> 52
Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys Ala Ile Ala
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Glu Glu Met Cys
20

<210> 53
<211> 23
<212> PRT
<213> *Homo sapiens*

<400> 53

Val Val Val Val Ser Thr Thr Gly Thr Gly Asp Pro Pro Asp Thr Ala
1 5 10 15
Arg Lys Phe Val Lys Glu Ile
20

<210> 54
<211> 29
<212> PRT
<213> Homo sapiens

<400> 54
Ala His Leu Arg Tyr Gly Leu Leu Gly Leu Gly Asp Ser Glu Tyr Thr
1 5 10 15
Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp Lys Arg Leu
20 25

<210> 55
<211> 19
<212> PRT
<213> Homo sapiens

<400> 55
Leu Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro
1 5 10 15
Gly Lys Leu

<210> 56
<211> 14
<212> PRT
<213> Homo sapiens

<400> 56
Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr Thr
1 5 10

<210> 57
<211> 17
<212> PRT
<213> Homo sapiens

<400> 57
Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu Val Ala Ser
1 5 10 15
Val

<210> 58
<211> 22
<212> PRT
<213> Homo sapiens

<400> 58
Ile Pro Ile Ile Met Val Gly Pro Gly Thr Gly Ile Ala Pro Phe Ile
1 5 10 15
Gly Phe Leu Gln His Arg
20

<210> 59
<211> 6
<212> PRT
<213> Homo sapiens

<400> 59
Ser Phe Ser Arg Asp Ala
1 5

<210> 60
<211> 41
<212> PRT
<213> Homo sapiens

<400> 60
Ala Pro Ala Lys Tyr Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln
1 5 10 15
Val Ala Arg Ile Leu Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly
20 25 30
Asp Ala Lys Asn Met Ala Lys Asp Val
35 40

<210> 61
<211> 9
<212> PRT
<213> Homo sapiens

<400> 61
Lys Arg Tyr Leu Gln Asp Ile Trp Ser
1 5